

SEQ ID NO: 19

**RESULT** 7  
**G28289/c**  
**LOCUS** G28289 383 bp DNA STS 29-JUN-1996  
**DEFINITION** human STS SHGC-34439, sequence tagged site.  
**ACCESSION** G28289  
**VERSION** G28289.1 GI:1397008  
**KEYWORDS** STS; STS sequence; primer; sequence tagged site.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 383)  
**AUTHORS** Myers, R.M.  
**JOURNAL** Unpublished (1996)  
**COMMENT**  
Contact: Richard M. Myers  
Stanford Human Genome Center (SHGC)  
Stanford University School of Medicine  
Department of Genetics, M-344, Stanford, CA 94305, USA  
Tel: 4157259687  
Fax: 4157259689  
Email: myers@shgc.stanford.edu  
  
**Primer A:** CCACTGGCTAGAAGCCCTG  
**Primer B:** TACCCACTGACTTCCAATCA  
**STS size:** 126  
**PCR Profile:**  
Initial incubation: 94 degrees C for 90 seconds  
  
Denaturation: 94 degrees C for 15 seconds  
Annealing: 62 degrees C for 23 seconds  
Polymerization: 72 degrees C for 30 seconds  
PCR Cycles: 30  
Thermal Cycler: Perkin Elmer 9600  
**Protocol:**  
Template: 25 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Taq Polymerase: 0.05 units/uL  
Total Vol: 10 uL  
  
**Buffer:**  
MgCl<sub>2</sub>: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.3  
  
Prepared with primer pairs provided by Sandoz, derived from H4114  
-- Washington University/Merck EST sequence.  
**FEATURES** Location/Qualifiers  
**source** 1. .383  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/map="12"  
**STS** 21. .146  
**primer\_bind** 21. .39  
**primer\_bind** complement(125. .146)  
**BASE COUNT** 101 a 73 c 95 g 107 t 7 others  
**ORIGIN**

```

Query Match           27.3%; Score 313.2; DB 54; Length 383;
Best Local Similarity 94.9%; Pred. No. 1.3e-82;
Matches 352; Conservative 0; Mismatches 15; Indels 4; Gaps 3;

Qy      251 ttacactggatgtg-ctagagactgactgcc--atgtgctcagaagaaggcatggcaag 307
       ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      371 TAACACTGGATGTGCCAGAGACTGACTGCCATGTGCCCTCAGAAAGAAGGCATGGCNAG 312

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Qy 308 actgtggaatgaggatattttgaatcagttatggtaatgcggaaatatttata 367
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |
Db 311 ACTGTGGAAATGAGGATATTNTTGAATCAGTTATGGTCATGCCAAGCAATACTTATA 252

Qy 368 tgaacaacccaagttagttctat tagctgcttataactgtactcttcggccagttt 427
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |
Db 251 TGAANAAACCCAAAGTAGAGTTCTATTTAGCTGCTTATAACTGTACTCTCGCCAGTTT 192

Qy 428 caaaaaaaaaaaaaagatttacatgacgtgccctgactgcccaagctccataccactgactctt 487
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |
Db 191 CAAAAAAAAGATTACATGACGTGCCCTGACTGCCNAAGCTCCATACCCACTGACTCTT 132

Qy 488 ccaatcaccaagtgtggaggctgccaccgagttcttgcggaaatacaacaatgagaaca 547
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |
Db 131 CCAATCACCAAGTGCTGGAGGCTGCCACCGAGTCTTGCAGAAATACAACATGAGAAC 72

Qy 548 catccaagcagtatttctcttcaagtca-ccagggttcttagccagtgggtggtcggc 606
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |
Db 71 CATCCAAGCAGTATTCTCTCTTCAAAGTCACCCAGGGCTCTAGCCAGTGGGANNTNGGC 12

Qy 607 cttttttactt 617
||| ||| ||| ||| |
Db 11 CCTTCTTACTT 1

```

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RESULT      3
N39010
LOCUS      N39010      542 bp      mRNA          EST      19-JAN-1996
DEFINITION yv22a08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
IMAGE:243446 3', mRNA sequence.
ACCESSION  N39010
VERSION    N39010.1  GI:1162217
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 542)
AUTHORS    Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
           ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
           Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
           ,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE      The WashU-Merck EST Project
JOURNAL    Unpublished (1995)
COMMENT    Contact: Wilson RK
           Washington University School of Medicine
           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: est@watson.wustl.edu
           High quality sequence stops: 476
           Source: IMAGE Consortium, LLNL
           This clone is available royalty-free through LLNL ; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.
           Seq primer: m13 -40 forward
           High quality sequence stop: 476.
FEATURES   Location/Qualifiers
source     1..542
           /organism="Homo sapiens"
           /db_xref="GDB:3792579"
           /db_xref="taxon:9606"
           /clone="IMAGE:243446"
           /clone_lib="Soares fetal liver spleen 1NFLS"
           /sex="male"
           /dev_stage="20 week-post conception fetus"
           /lab_host="DH10B (ampicillin resistant)"
           /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
           with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;

```

1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAAGAATTAAATTAAAGATCTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT        135 a     159 c     123 g     124 t     1 others  
ORIGIN

Query Match                  42.4%; Score 486.4; DB 159; Length 542;  
Best Local Similarity    99.6%; Pred. No. 1.1e-133;  
Matches 498; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy    647 gtactaaatcccaggccagcagctgtcaacttcagtcccgactctgtgcctgtggc 706  
Db    1 GTACTAAATCCCAGGCCAGCAGCTGTCACCTCAGTCCTCCGACTCTGTGCCTGTTGGTC 60

Qy    707 tttgcaaagggttctctgactcgaacacacactggaaaaagttgtctctgtgact 766  
Db    61 TTTGCAAAGGTTCTCTGACTCGAACACACTGGAAAAGTTGTCTCTGTGACTTGTGACT 120

Qy    767 tcttgaatcacaggctccagccactgaaatctgtgttaaccagaaaccta 826  
Db    121 TCTTTGAATCACAGGCCAG-CACTGGAAGTAAAAACTCTGCTGTTAACAGAAACCTA 179

Qy    827 caaacctcccaagggtgaaatcccagcagaaaaacacccccccaacagactccccct 886  
Db    180 CAAACCTTCCAAGGTGGAAGAATCCAGCAGAAAAACACCCCCCAACAGACTCCCCCT 239

Qy    887 ccaaagctggccaagaggatctgtccatatcttcctgacttgatgataaaaattccc 946  
Db    240 CCAAAGCTGGCCAAGAGGATCTGTCCAATATCTTCCTGACTGGATGATAAAAATTCCC 299

Qy    947 agaaaaaggccctcaggaggccttcctgtgcattggacctaaccacgaatccccagg 1006  
Db    300 AGGAAAAGGGCCCTCAGGAGGCCTTCTGTGCATCTGGACCTAACGAAATCCCCAGG 359

Qy    1007 gagaaaccctggatatttccttccttcctggagccatggaggagaactgggtgtcc 1066  
Db    360 GAGAAACCCCTGGATATTCCTTCCTTCCTGGAGCCTATGGAGGAGAAGCTGGTTGTCC 419

Qy    1067 tgcctttcccaaaagaaaaagcacgcactgctgagtgccaggccagccagaatgcc 1126  
Db    420 TGCCTTTCCCCAGAGAAAAAGCACCGACTGCTGAGTGCCAGGGCCAGCCAGAACGCC 479

Qy    1127 gccctctgtcctccgcca 1146  
Db    480 GCCCTCTGTCCCTCCGCCA 499

SEQ ID NO: 37

RESULT 10  
G27766/c  
LOCUS      G27766        503 bp      DNA      STS      29-JUN-1996  
DEFINITION human STS SHGC-33193, sequence tagged site.  
ACCESSION G27766  
VERSION     G27766.1 GI:1396485  
KEYWORDS    STS; STS sequence; primer; sequence tagged site.  
SOURCE      human.  
ORGANISM    Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 503)



Db	264	GCGATGGGACGATGGACAGAGACAGAGCGTGCANACGTAGAGTGGCTAGTGAAGGACGC	205
Qy	1297	cttttgactcttcttggctcagcatgttactggattggaaataatgagactgagcc	1356
Db	204	CTTTTGACTCTTCTTGGCTCAGCATGTTGACTGGATTGAAATAATGAGACTGA-NC	146
Qy	1357	ctcggcttggctgcacttacccctgtacactgccttgcacccgtacactgcaccc	1416
Db	145	CTCGGCTTGGGCTGCACCTCACCCGTANACTGCCTTGTACCCGTGAGCTGCATCACCTCC	86
Qy	1417	taaaactgaggcagtc-tcataccatggagagatgcctctttagtgcatttcagccac-tcac	1474
Db	85	TAAAATGAGCAGTCTTCATACCATGGAGAGATGCCTCTCTTATGTCTTCAGCCACGTCAC	26
Qy	1475	ttataaaagatacttatctttcagc	1499
Db	25	TTATAAAAGATACTTCNCTTTCAAGC	1

09445258Results

RESULT 5  
A2HS\_HUMAN  
ID A2HS\_HUMAN STANDARD; PRT; 367 AA.  
AC P02765; O14962; O14961;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-APR-1988 (Rel. 07, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A) (ALPHA-2-Z-GLOBULIN)  
DE (BA-ALPHA-2-GLYCOPROTEIN).  
GN AHSG OR FETUA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87260816; PubMed=3474608;  
RA Lee C.-C., Bowman B.H., Yang F.;  
RT "Human alpha 2-HS-glycoprotein: the A and B chains with a connecting  
RT sequence are encoded by a single mRNA transcript.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:4403-4407(1987).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97464058; PubMed=9322749;  
RA Osawa M., Umetsu K., Sato M., Ohki T., Yukawa N., Suzuki T.,  
RA Takeichi S.;  
RT "Structure of the gene encoding human alpha 2-HS glycoprotein  
RT (AHSG).";  
RL Gene 196:121-125(1997).  
RN [3]  
RP SEQUENCE OF 19-300.  
RX MEDLINE=86111834; PubMed=3944104;  
RA Yoshioka Y., Gejyo F., Marti T., Rickli E.E., Burgi W., Offner G.D.,  
RA Troxler R.F., Schmid K.;  
RT "The complete amino acid sequence of the A-chain of human plasma  
RT alpha 2HS-glycoprotein.";  
RL J. Biol. Chem. 261:1665-1676(1986).  
RN [4]  
RP SEQUENCE OF 341-367.  
RX MEDLINE=83161108; PubMed=6833285;  
RA Gejyo F., Chang J.-L., Burgi W., Schmid K., Offner G.D., Troxler R.F.,  
RA van Halbeek H., Dorland L., Gerwig G.J., Vliegenthart F.G.;  
RT "Characterization of the B-chain of human plasma alpha  
RT 2HS-glycoprotein. The complete amino acid sequence and primary  
RT structure of its heteroglycan.";  
RL J. Biol. Chem. 258:4966-4971(1983).  
RN [5]  
RP DISULFIDE BONDS.  
RX MEDLINE=89150282; PubMed=2645941;  
RA Araki T., Yoshioka Y., Schmid K.;  
RT "The position of the disulfide bonds in human plasma alpha 2 HS-  
RT glycoprotein and the repeating double disulfide bonds in the domain  
RT structure.";  
RL Biochim. Biophys. Acta 994:195-199(1989).  
RN [6]  
RP DISULFIDE BONDS.  
RX MEDLINE=89340518; PubMed=2760061;  
RA Kellerman J., Haupt H., Auerswald E.-A., Mueller-Esterl W.;  
RT "The arrangement of disulfide loops in human alpha 2-HS glycoprotein.  
RT Similarity to the disulfide bridge structures of cystatins and  
RT kininogens.";  
RL J. Biol. Chem. 264:14121-14128(1989).  
RN [7]  
RP SEQUENCE OF 34-367 FROM N.A., AND VARIANT AHSG\*2.  
RC TISSUE=Liver;  
RX MEDLINE=97157105; PubMed=9003486;  
RA Osawa M., Umetsu K., Ohki T., Nagasawa T., Suzuki T., Takeichi S.;  
RT "Molecular evidence for human alpha 2-HS glycoprotein (AHSG)  
RT polymorphism.";

RL Hum. Genet. 99:18-21(1997).  
 CC -!- FUNCTION: PROMOTES ENDOCYTOSIS, POSSESSES OPSONIC PROPERTIES AND  
 CC INFLUENCES THE MINERAL PHASE OF BONE. SHOWS AFFINITY FOR CALCIUM  
 CC AND BARIUM IONS.  
 CC -!- SUBUNIT: ALPHA-2-HS GLYCOPROTEIN DERIVES FROM THIS PRECURSOR,  
 CC WHEN THE CONNECTING PEPTIDE IS CLEAVED OFF. THE TWO CHAINS A AND  
 CC B ARE HELD TOGETHER BY A SINGLE DISULFIDE BOND.  
 CC -!- SUBCELLULAR LOCATION: SECRETED.  
 CC -!- TISSUE SPECIFICITY: SYNTHESIZED IN LIVER AND SELECTIVELY  
 CC CONCENTRATED IN BONE MATRIX. IT IS ALSO FOUND IN DENTIN IN MUCH  
 CC HIGHER QUANTITIES THAN OTHER PLASMA PROTEINS.  
 CC -!- POLYMORPHISM: THERE ARE TWO COMMON ALLELES, AHSG\*1 AND AHSG\*2.  
 CC AHSG\*1 HAS THR-248 AND THR-256; AHSG\*2 HAS MET-248 AND SER-256.  
 CC -!- SIMILARITY: BELONGS TO THE FETUIN FAMILY.  
 CC -!- SIMILARITY: CONTAINS 2 CYSTATIN-LIKE DOMAINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL; M16961; AAA51683.1; -.  
 DR EMBL; D67013; BAA22652.1; -.  
 DR EMBL; D67012; BAA22651.1; -.  
 DR PIR; A29081; WOHU.  
 DR PIR; S04467; S04467.  
 DR PIR; S02765; S02765.  
 DR GlycoSuiteDB; P02765; -.  
 DR CarbBank; CCSD:11752; -.  
 DR CarbBank; CCSD:36455; -.  
 DR SWISS-2DPAGE; P02765; HUMAN.  
 DR MIM; 138680; -.  
 DR InterPro; IPR000010; -.  
 DR InterPro; IPR001363; -.  
 DR Pfam; PF00031; cystatin; 2.  
 DR PROSITE; PS01254; FETUIN\_1; 1.  
 DR PROSITE; PS01255; FETUIN\_2; 1.  
 KW Glycoprotein; Signal; Repeat; Plasma; Mineral balance; Polymorphism.  
 FT SIGNAL 1 18  
 FT CHAIN 19 300 ALPHA-2-HS-GLYCOPROTEIN, CHAIN A.  
 FT PEPTIDE 301 340 CONNECTING PEPTIDE.  
 FT CHAIN 341 367 ALPHA-2-HS-GLYCOPROTEIN, CHAIN B.  
 FT DOMAIN 27 144 CYSTATIN-LIKE 1.  
 FT DOMAIN 145 260 CYSTATIN-LIKE 2.  
 FT DISULFID 32 358 INTERCHAIN.  
 FT DISULFID 89 100  
 FT DISULFID 114 132  
 FT DISULFID 146 149  
 FT DISULFID 208 219  
 FT DISULFID 230 247  
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . ).  
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. . ).  
 FT CARBOHYD 256 256 O-LINKED (GALNAC. . ).  
 FT CARBOHYD 270 270 O-LINKED (GALNAC. . ).  
 FT CARBOHYD 346 346 O-LINKED (GALNAC. . ).  
 FT VARIANT 248 248 T -> M (IN AHSG\*2).  
 FT /FTId=VAR\_002388.  
 FT VARIANT 256 256 T -> S (IN AHSG\*2).  
 FT /FTId=VAR\_002389.  
 FT CONFLICT 16 16 C -> W (IN REF. 2).  
 FT CONFLICT 54 54 W -> K (IN REF. 3).  
 FT CONFLICT 125 125 F -> S (IN REF. 7).  
 FT CONFLICT 204 204 S -> C (IN REF. 2).  
 SQ SEQUENCE 367 AA; 39324 MW; 1AAF0C8D6B7E2789 CRC64;

Query Match 13.6%; Score 274; DB 1; Length 367;  
 Best Local Similarity 26.2%; Pred. No. 4.2e-13;

RESULT 6  
A2HS\_RABIT  
ID A2HS\_RABIT STANDARD; PRT; 360 AA.  
AC P80191; O18997;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-OCT-2000 (Rel. 40, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A) (HAEMONECTIN) (FRAGMENT).  
GN AHSG OR FETUA.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NEW ZEALAND WHITE; TISSUE=Liver;  
RA Osawa M., Saito T., Takeichi S.;  
RT "Nucleotide sequence of cDNA encoding rabbit fetuin.";  
RL Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE OF 19-26; 55-62; 118-128; 235-250 AND 332-344.  
RC STRAIN=NEW ZEALAND WHITE; TISSUE=Bone marrow;  
RX MEDLINE=93238730; PubMed=7682944;  
RA White H., Totty N., Panayotou G.;  
RT "Haemonectin, a granulocytic-cell-binding protein, is related to the plasma glycoprotein fetuin.";  
RL Eur. J. Biochem. 213:523-528(1993).  
CC -!- FUNCTION: A CELL ADHESION PROTEIN THAT BINDS IMMATURE CELLS OF THE GRANULOCYTE LINEAGE.  
CC -!- SUBCELLULAR LOCATION: SECRETED.  
CC -!- TISSUE SPECIFICITY: BONE MARROW.  
CC -!- SIMILARITY: BELONGS TO THE FETUIN FAMILY.  
CC -!- SIMILARITY: CONTAINS 2 CYSTATIN-LIKE DOMAINS.  
CC -----  
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 CC  
 DR EMBL; D67014; BAA22653.1; -.  
 DR PIR; S30340; S30340.  
 DR InterPro; IPR000010; -.  
 DR InterPro; IPR001363; -.  
 DR Pfam; PF00031; cystatin; 2.  
 DR PROSITE; PS01254; FETUIN\_1; 1.  
 DR PROSITE; PS01255; FETUIN\_2; 1.  
 KW Cell adhesion; Repeat; Glycoprotein; Signal.  
 FT NON\_TER 1 1  
 FT SIGNAL <1 15 BY SIMILARITY.  
 FT CHAIN 16 360 ALPHA-2-HS-GLYCOPROTEIN.  
 FT DOMAIN 24 141 CYSTATIN-LIKE 1.  
 FT DOMAIN 142 257 CYSTATIN-LIKE 2.  
 FT DISULFID 29 351 BY SIMILARITY.  
 FT DISULFID 86 97 BY SIMILARITY.  
 FT DISULFID 111 129 BY SIMILARITY.  
 FT DISULFID 143 146 BY SIMILARITY.  
 FT DISULFID 205 216 BY SIMILARITY.  
 FT DISULFID 227 244 BY SIMILARITY.  
 FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 126 126 S -> P (IN REF. 1).  
 SO SEQUENCE 360 AA; 38386 MW; F0908740610CBB95 CRC64;

Query Match 13.4%; Score 270.5; DB 1; Length 360;  
 Best Local Similarity 25.0%; Pred. No. 7.4e-13;  
 Matches 99; Conservative 51; Mismatches 181; Indels 65; Gaps 13;

RESULT 1  
US-08-737-045-14  
; Sequence 14, Application US/08737045A  
; Patent No. 5981483  
; GENERAL INFORMATION:  
; APPLICANT: Dennis, James W.  
; APPLICANT: Denetriou, Michael  
; APPLICANT: Mount Sinai Hospital Corporation

; TITLE OF INVENTION: COMPOSITIONS COMPRISING MODULATORS OF CYTOKINES OF THE  
; TITLE OF INVENTION: TGF $\beta$  SUPERFAMILY AND A METHOD OF TREATMENT WITH SUCH A  
; TITLE OF INVENTION: COMPOSITION (AS AMENDED)  
; FILE REFERENCE: 7933.94USWO  
; CURRENT APPLICATION NUMBER: US/08/737,045A  
; CURRENT FILING DATE: 1997-03-20  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 367  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-737-045-14

Query Match 13.6%; Score 274; DB 2; Length 367;  
Best Local Similarity 26.2%; Pred. No. 1.1e-19;  
Matches 102; Conservative 64; Mismatches 169; Indels 54; Gaps 17;

Qy 11 ILVLCCGAMSPPQLALNPSALLSR--GCNDSDVLAAGFALRINKDRKDGYVRLNRVN 68  
Db 5 VLLLCLAQLWGCHSAPHGPGLIYRQPNCDDPETEEAALVAIDYINQNLPWGYKHTLNQID 64

Qy 69 DAQEYRRGGGLGSLFYLTLDVLETDCVLRKKAWQDCGMRIFFE-SVYQQCK-AIFYMNNP 126  
Db 65 EVKVWPQQPSGELFEIEIDTLETTCHVLDPTVARCSVQLKEHAVEGDCDFQLLKLDGK 124

Qy 127 SRVLYLAAYNCLRPVSKKIYMTCPDCPSSIPTDSSNHQVLEAATESLAKYNNENTSKQ 186  
Db 125 FSVVYA---KCDSSPDSAEDVRKVQCDCPLLAPLNDT--RVVHAAKAALAAFNAQNNGSN 179

Qy 187 YSLFKVTRASSQWV-VGPSYFVEYLIKEPCT---KSQASSCSLQSSDSVPVGLCKGSLT 242  
Db 180 FQLEEISRA--QLVPLPPSTYVEFTVSGTDCVAKEATEAAKCNLAAEKQ--YGFCKATLS 235

Qy 243 RTHWEKFVSVTCDFESQAPATGSENSAVNQK-PTNLPKVEESQQKNTPTDPSKAGPR 301  
Db 236 EKLGGAEVAVTCTVFQTQPVTSQPQPEGANEAVPT---PVVDPDAPPSPPLGAPG-LPPA 291

Qy 302 GSVQYLPDLDDKNSQEKGPKQEAFPVHDL-----TTNPQGETLDISFLFLEPMEEK 352  
Db 292 GSP---PDSHVLLAAPPGHQ-LHRAHYDLRHTFMGVVSLGPSGE----- 332

Qy 353 LVVLPFPKEKARTAECPGPAQNAsPLVLP 381  
Db 333 ---VSHPR-KTRTVVQPSVGAAAGPVVPP 357

RESULT 4  
US-08-483-926A-10  
; Sequence 10, Application US/08483926A  
; Patent No. 5821227  
; GENERAL INFORMATION:  
; APPLICANT: Dennis, James W.  
; TITLE OF INVENTION: MODULATORS OF CYTOKINES OF THE TGF BETA  
; TITLE OF INVENTION: SUPERFAMILY AND METHODS FOR ASSAYING FOR SAME  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BERESKIN & PARR  
; STREET: 40 King Street West  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5H 3Y2  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/483,926A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kurdydyk, Linda M.  
; REGISTRATION NUMBER: 34,971  
; REFERENCE/DOCKET NUMBER: 3153-155  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 364-7311  
; TELEFAX: (416) 361-1398  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 364 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: Sheep  
US-08-483-926A-10

Query Match 13.2%; Score 265.5; DB 2; Length 364;  
Best Local Similarity 29.5%; Pred. No. 7.7e-19;  
Matches 92; Conservative 49; Mismatches 136; Indels 35; Gaps 15;

QY 7 LALCILVLCCGAMSPPQLALNPSA-LLSRGCNDSDVLAAGFALRDINKDRKDGYVLRLN 65  
| | : || | : | : | | : | | : | | : || | | | | |  
Db 6 LLFCLAQLC---SCRSIPLDPIAGYKEPACDDPDTEQAALAAVDYINKHLPGRYKHTLN 61

QY 66 RVNDAQEYRRGGLGSILFYLTLDVLETDCHVLRKKAWQDCGMRIFFE-SVYQCKA-IFYM 123  
::: : | | : : | | : | | | | | | : | : | | : | | : |  
Db 62 QIDSVKVWP RRPTGEVYDIEIDTLETTCHVLDP TLVNCVRQQTEHAVEGDCDIHVLKQ 121

QY 124 NNPSRVLYLAAYNCTLRPVSKKKIYMTCPDCPSSIPTDSSNHQVLEAATESLAKYNNENT 183  
: | | : | | | : : | | | | | | : | | : | | : | | : |  
Db 122 DGQFSVLF---KCDSSPDSAEDVRKLCPDCPLLAPL--NNSQVVHAAEVALATFNAQNN 176

Qy 184 SKQYSLFKVTRASSQWVVG-P-SYFVEYLIKESPCTKSQA---SSCSLQSSDSVPVGLCKG 239  
: | ::|| | : | | | | : | : | : | : | : | | | | | |  
Db 177 GSYFQLVEISRA--QFVPLPGSVSVEFAVAATDCIAKEVVDPDKCNLLAEKQ--YGFCKG 232

Qy 240 S-LTRTHWEKFVSVTCDFES----QAPATGSENSAVNQKPTNLPKVEESQQKNTPPTD 293  
| : : | : | | | : | : | | | | : | : | : | : |  
Db 233 SVIQKALGGEDVTCTLFQTQPVIPQPQPEGAEAGA---PSAVPDAAVPD---AAVP 284

Qy 294 SPSKAG-PRGSV 304  
: | | | | | |  
Db 285 APSAAGLPVGSV 296

RESULT 15  
US-08-193-114B-1  
; Sequence 1, Application US/08193114B  
; Patent No. 5472945  
; GENERAL INFORMATION:  
; APPLICANT: Schmaier, Alvin H.  
; APPLICANT: Jiang, Yongping  
; TITLE OF INVENTION: Modulation of Blood  
; TITLE OF INVENTION: Pressure and Inhibition of Platelet Activation  
; TITLE OF INVENTION: with Kininogen Fragment  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seidel, Gonda, Lavorgna &  
; ADDRESSEE: Monaco, P.C.  
; STREET: 1800 Two Penn Center Plaza  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/193,114B  
; FILING DATE: 9 February 1994  
; CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. Application  
; APPLICATION NUMBER: Serial No. 5472945 07/744,545  
; FILING DATE: 13 August 1991  
ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 6056-137 CII  
TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-8383  
; TELEFAX: (215) 568-5549  
; TELEX: No. 5472945e  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
; LENGTH: 117 amino acids  
; TYPE: peptide  
; TOPOLOGY: linear  
US-08-193-114B-1

Query Match 6.4%; Score 129.5; DB 1; Length 117;  
Best Local Similarity 30.4%; Pred. No. 1e-05;  
Matches 35; Conservative 18; Mismatches 43; Indels 19; Gaps 6;

Qy 151 CPDCPSSIPTDSSNHQVLEAATESLAKYNNENTSKQY-SLFKVTRASSQWVGPSYFVEY 209  
| || ||||:| ::| | :| ||| :| :| :| | | | ||:::  
Db 1 CVGCPRDIPPTNSP--ELEETLTHTITKLNAENNATFYFKIDNVKKARVQVVAGKKYFIDF 58

Qy 210 LIKESPCTKSQ---ASSCSL---QSSDSVPVGLCKGSLTRTHWEK--FVSVTC 254  
: :|: |:| ||| ||| | :| ||| :| |  
Db 59 VARETTCSKESNEELTESCETKKLGQSLD-----CNAEVYVVPWEKKIYPTVNC 107